

A partial sequence of the NS5 gene showed that the Zika virus isolate from this patient was closely related to those described elsewhere in the Western Hemisphere belonging to the Asian lineage, particularly to 2 strains identified in Brazil and Suriname during 2015.

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The findings and conclusions in this report are those of the authors and do not necessarily represent the official opinion of the Ministry of Health of Mexico.

### References

1. Musso D, Cao-Lormeau VM, Gubler DJ. Zika virus: following the path of dengue and chikungunya? *Lancet*. 2015;386:243–4 [http://dx.doi.org/10.1016/S0140-6736\(15\)61273-9](http://dx.doi.org/10.1016/S0140-6736(15)61273-9).
2. Musso D. Zika virus transmission from French Polynesia to Brazil. *Emerg Infect Dis*. 2015;21:1887 <http://dx.doi.org/10.3201/eid2110.151125>.
3. Kuno G, Chang GJ. Full-length sequencing and genomic characterization of Bagaza, Kedougou, and Zika viruses. *Arch Virol*. 2007;152:687–96. <http://dx.doi.org/10.1007/s00705-006-0903-z>
4. Haddow AD, Schuh AJ, Yasuda CY, Kasper MR, Heang V, Huy R, et al. Genetic characterization of Zika virus strains: geographic expansion of the Asian lineage. *PLoS Negl Trop Dis*. 2012;6:e1477 <http://dx.doi.org/10.1371/journal.pntd.0001477>.
5. Enfissi A, Codrington J, Roosblad J, Kazanji M, Rousset D. 2016. Zika virus genome from the Americas. *Lancet*. 2016;387:227–8. [http://dx.doi.org/10.1016/S0140-6736\(16\)00003-9](http://dx.doi.org/10.1016/S0140-6736(16)00003-9)
6. World Health Organization. Zika virus outbreaks in the Americas. *Wkly Epidemiol Rec*. 2015;90:609–10. <http://www.who.int/wer/2015/wer9045.pdf?ua=1>
7. Centers for Disease Control and Prevention. Zika virus [cited 2016 Jan 20]. <http://www.cdc.gov/zika/>
8. Untergasser A, Nijveen H, Rao X, Bisseling T, Geurts R, Leunissen JA. Primer3Plus, an enhanced web interface to Primer3. *Nucleic Acids Res*. 2007;35:W71–4. <http://dx.doi.org/10.1093/nar/gkm306>
9. Díaz-Quinonez JA, Escobar-Escamilla N, Ortiz-Alcántara J, Vázquez-Pichardo M, de la Luz Torres-Rodríguez M, Nuñez-León A, et al. Identification of Asian genotype of chikungunya virus isolated in Mexico. *Virus Genes*. 2016; 52:127–9. <http://dx.doi.org/10.1007/s11262-015-1275-9>

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## Technological Solutions to Address Drug-Resistant *Neisseria gonorrhoeae*

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**To the Editor:** Since the 1930s, *Neisseria gonorrhoeae* has become resistant to drugs in every class of antimicrobial therapy used to treat it. We read with interest the article by Martin et al. about trends in Canada on *N. gonorrhoeae* susceptibility to third-generation cephalosporins, the only class of antimicrobial drugs to which most *N. gonorrhoeae* strains remain susceptible (1). We find the reported decrease in cefixime- and ceftriaxone-reduced susceptibility during 2010–2014 encouraging, but remain concerned about a threat from drug-resistant and untreatable *N. gonorrhoeae* infections: a similar downward trend in the United States reversed in 2014 (2). That divergence demonstrates the limited reliability of surveillance data.

Addressing resistance requires new methods for susceptibility determination without culture. Real-time screening for genes associated with antimicrobial drug resistance, such as *penA* mosaic alleles yielding decreased susceptibility to oral extended-spectrum cephalosporins, may be a valuable method to determine treatment (3). In the same issue of *Emerging Infectious Diseases*, Deguchi et al. described a case of multidrug-resistant *N. gonorrhoeae* (4), further highlighting the urgency for the innovative approach of using molecular tests to individualize treatment regimens. An ongoing study supported by the National Institutes of Health (R21AI109005) is evaluating how a laboratory-developed molecular *N. gonorrhoeae* genotypic susceptibility test for ciprofloxacin enables rapid identification of effective antimicrobial drugs (5).

*N. gonorrhoeae* may acquire new resistance mechanisms under selection pressures imposed by use of antimicrobial drugs and horizontal gene transfer from other commensal *Neisseria* species resident in the human oropharynx (3). Inconsistent pharyngeal *N. gonorrhoeae* screening may lead to missed opportunities for treatment. A National Institutes of Health program (Antibiotic Resistance Leadership Group, award no. UM1AI104681) is ongoing to assist manufacturers in obtaining US Food and Drug Administration approval for molecular assays to detect extragenital gonococcal infections.

For nearly 8 decades, *N. gonorrhoeae* has been controllable. Continued investment in research and the development of new laboratory technology are critical in supporting an effective response to mitigate the threat of untreatable gonorrhea.

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## References

1. Martin I, Sawatzky P, Liu G, Allen V, Lefebvre B, Hoang L, et al. Decline in decreased cephalosporin susceptibility and increase in azithromycin resistance in *Neisseria gonorrhoeae*, Canada. *Emerg Infect Dis*. 2016;22:65–7. <http://dx.doi.org/10.3201/eid2201.151247>
2. Kirkcaldy RD, Hook EW III, Soge OO, del Rio C, Kubin G, Zenilman JM, et al. Trends in *Neisseria gonorrhoeae* susceptibility to cephalosporins in the United States, 2006–2014. *JAMA*. 2015;314:1869–71. <http://dx.doi.org/10.1001/jama.2015.10347>
3. Buono SA, Watson TD, Borenstein LA, Klausner JD, Pandori MW, Godwin HA. Stemming the tide of drug-resistant *Neisseria gonorrhoeae*: the need for an individualized approach to treatment. *J Antimicrob Chemother*. 2015;70:374–81. <http://dx.doi.org/10.1093/jac/dku396>
4. Deguchi T, Yasuda M, Hatazaki K, Kameyama K, Horie K, Kato T, et al. New clinical strain of *Neisseria gonorrhoeae* with decreased susceptibility to ceftriaxone, Japan. *Emerg Infect Dis*. 2016;22:142–4. <http://dx.doi.org/10.3201/eid2201.150868>
5. Hemarajata P, Yang S, Soge OO, Humphries RM, Klausner JD. Performance and verification of a real-time PCR assay targeting *gyrA* gene for prediction of ciprofloxacin resistance in *Neisseria gonorrhoeae*. *J Clin Microbiol*. 2016;54:805–8. <http://dx.doi.org/10.1128/JCM.03032-15>

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## Detection of Zika Virus in Semen

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**To the Editor:** As an increasing number of autochthonous Zika virus infections are reported from several South America countries (1), we read with interest the report from Musso et al. on the potential sexual transmission of Zika virus (2). We report additional evidence for this potential route of transmission after identification of an imported case of infection into the United Kingdom.

After an outbreak alert for Zika in French Polynesia, active screening was implemented at Public Health England (Porton Down, United Kingdom). In 2014, a 68-year-old man had onset of fever, marked lethargy, and an erythematous rash 1 week after returning from the Cook Islands. Serum samples taken 3 days into the febrile illness tested negative for dengue and chikungunya viruses by real-time reverse transcription PCR (rRT-PCR). Test results for dengue virus IgM and chikungunya virus IgM also were negative; a test result for dengue virus IgG was indeterminate.

An rRT-PCR test result for Zika virus (3) was positive and indicated a crossing threshold value of 35 cycles. This low viral load, commonly observed even in the acute phase of disease (3), meant that attempts to obtain sequence data were unsuccessful. Convalescent-phase serum, urine, and semen samples were requested; only semen was positive for by rRT-PCR, at 27 and 62 days after onset of febrile illness. These results demonstrated stronger signals than those obtained in tests of the original serum sample, with crossing threshold values of 29 and 33 cycles, respectively. Zika virus-specific plaque reduction neutralization test results were positive on convalescent-phase serum samples.

Although we did not culture infectious virus from semen, our data may indicate prolonged presence of virus in semen, which in turn could indicate a prolonged potential for sexual transmission of this flavivirus. Moreover, these findings could inform decisions regarding what control methods are implemented and which specimen types are best suited for diagnostic detection.

## References

1. Pan American Health Organization. Reported increase of congenital microcephaly and other central nervous system symptoms—epidemiological update [cited 2016 Feb 4]. [http://www.paho.org/hq/index.php?option=com\\_content&view=article&id=1239&Itemid=2291&lang=en](http://www.paho.org/hq/index.php?option=com_content&view=article&id=1239&Itemid=2291&lang=en)
2. Musso D, Roche C, Robin E, Nhan T, Teissier A, Cao-Lormeau V-M. Potential sexual transmission of Zika virus. *Emerg Infect Dis*. 2015;21:359–61. <http://dx.doi.org/10.3201/eid2102.141363>
3. Lanciotti RS, Kosoy OL, Laven JJ, Velez JO, Lambert AJ, Johnson AJ, et al. Genetic and serologic properties of Zika virus associated with an epidemic, Yap State, Micronesia, 2007. *Emerg Infect Dis*. 2008;14:1232–9. <http://dx.doi.org/10.3201/eid1408.080287>

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